

1/32

FIG. 1A

Input file Fbh56919FL2.seq
Sequence length 3003

```

TTCGGCACCAAGCTGCTGCGGGGGAGCTTTCTGAGGTACTGTGGAGCACCCAAAGTCTGTGAGCCCTCTGGCCGTGC
AARACAGCCACAGAGGAAACAGACCTTGCTTATTACCCACAGCCCTGGGACGTCTCTCCAGAGTCTCCATCAGCTT
TGCTAATCGACTGATTTGGAAATAATTCCTCAACACACCAAGTCARAGGATACAGGAGCAGCGGCTCCCTGTTGTAT
GGACATTCTGCACCCGAACTAGCTGAGTCTCCTGAAGTTTATGTTATGAACAGAGAACTTTCATCCACGACAT
M D E S A L T L G T I D V
GATTTGGGAATACACTTTGTGAC ATG GAT GAA TCT GCA CTG ACC CTT GET ACA ATA GAT GTT
S Y L P H S S E Y S V G R C K H T S E E
TCT TAT CTG CCA CAT TCA TCA GAA TAC AGT GTT GGT CGA TGT AGG CAC ACA AGT GAG GAA
W G E C G F R P T V F R S A T L K W K E
TGG GGT GAG TGT GGC TTT AGA CCC ACC GTC TTC AGA TCT GCA ACT TTA AAA TGG AAA GAA
S L M S R K R P F V G R C C Y S C T P Q
AGC CTA ATG AGT CGG AAA AGG CCA TTT GTT GGA AGA TGT TAC TCC TGC ACT CCC CAG
S W D K F F N P S I P S L G L R N V I Y
AGC TGG GAC AAA TTT TTC AAC CCC AGT ATC CCG TCT TTG GGT TTG CGG AAT GTT ATT TAT
I N E T H T R H R G W L A R R L S Y V L
ATC AAT GAA ACT CAC ACA AGA CAC CGC GGA TGG CTT GCA AGA CGC CTT TCT TAC GTT CTT
F I Q E R D V H K G M F A T N V T E N V
TTT ATT CAA GAG CGA GAT GTG CAT AAG GGC ATG TTT GCC ACC AAT GTG ACT GAA AAT GTG

```

13

39

33

99

53

159

73

219

93

279

113

339

133

399

2/32

FIG. 1B

153 L N S S R V Q E A I A E V A A E L N P D
 459 CTG AAC AGC AGT AGA GTA CAA GAG GCA ATT GCA GAA GTG GCT GCT GAA TTA AAC CCT GAT
 173 G S A Q Q Q S K A V N K V K K A K R I
 519 GGT TCT GCC CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT
 193 L Q E M V A T V S P A M I R L T G W V L
 579 CTT CAA GAA ATG ATG GCT GCC ACT GTC TCA CCG GCA ATG ATC AGA CTG ACT GSG TGG GTG CTG
 213 L K L F N S F F W N I Q I H K G Q L E M
 639 CTA AAA CTG TTC AAC AGC TTC TTT TGG AAC ATT CAA ATT CAC AAA GGT CAA CTT GAG ATG
 233 V K A A T E T N L P L L F L P V H R S H
 699 GTT AAA GCT GCA ACT GAG ACG AAT TTG CCG CTT CTG TTT CTA CCA GTT CAT AGA TCC CAT
 253 I D Y L L L T F I L F C H N I K A P Y I
 759 ATT GAC TAT CTG CTG CTC ACT TTC ATT CTC TTC TGC CAT AAC ATC AAA GCA CCA TAC ATT
 273 A S G N N L N I P I F S T L I H K L G G
 819 GCT TCA GGC AAT AAT CTC AAC ATC CCA ATC TTC AGT ACC TTG ATC CAT AAG CTT GSG GGC
 293 F F I R K R L D E T P D G R K D V L Y R
 879 TTC TTC ATA CGA AGG CTC GAT GAA ACA CCA GAT GGA CGG AAA GAT GTT CTC TAT AGA
 313 A L L H G H I V E L L R Q Q Q F L E I F
 939 GCT TTG CTC CAT GSG CAT ATA GTT GAA TTA CTT CGA CAG CAG CAA TTC TTG GAG ATC TTC
 333 L E G T R S R S G K T S C A R A G L L S
 999 CTG GAA GGC ACA CTT TCT AGG AGT GGA AAA ACC TCT TGT GCT CGG GCA GGA CTT TTG TCA

3/32

FIG. 1C

| | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| V | V | V | D | T | L | S | T | N | V | I | P | D | I | L | I | I | P | V | G | 353 |
| GTT | GTG | GTA | GAT | ACT | CTG | TCT | ACC | AAT | GTC | ATC | CCA | GAC | ATC | TTG | ATA | ATA | CCT | GTT | GGA | 1059 |
| I | S | Y | D | R | I | I | E | G | H | Y | N | G | E | Q | L | G | K | P | K | 373 |
| ATC | TCC | TAT | GAT | CGC | ATT | ATC | GAA | GGT | CAC | TAC | AAT | GGT | GAA | CAA | CTG | GGC | AAA | CCT | AAG | 1119 |
| K | N | E | S | L | W | S | V | A | R | G | V | I | R | M | L | R | K | N | Y | 393 |
| AAG | AAT | GAG | AGC | CTG | TGG | AGT | GTA | GCA | AGA | GGT | GTT | ATT | AGA | ATG | TTA | CGA | AAA | AAC | TAT | 1179 |
| G | C | V | R | V | D | F | A | Q | P | F | S | L | K | E | Y | L | E | S | Q | 413 |
| GGT | TGT | GTC | CGA | GTG | GAT | TTT | GCA | CAG | CCA | TTT | TCC | TTA | AAG | GAA | TAT | TTA | GAA | AGC | CAA | 1239 |
| S | Q | K | P | V | S | A | L | L | S | L | E | Q | A | L | L | P | A | I | L | 433 |
| AGT | CAG | AAA | CCG | GTG | TCT | GCT | CTA | CTT | TCC | CTG | CAG | CAA | GCG | TTG | TTA | CCA | GCT | ATA | CTT | 1299 |
| P | S | R | P | S | D | A | A | D | E | G | R | D | T | S | I | N | E | S | R | 453 |
| CCT | TCA | AGA | CCC | AGT | GAT | GCT | GCT | GAT | GAA | GGT | AGA | GAC | ACG | TCC | ATT | AAT | GAG | TCC | AGA | 1359 |
| N | A | T | D | E | S | L | R | R | L | I | A | N | L | A | E | H | I | L | L | 473 |
| AAT | GCA | ACA | GAT | GAA | TCC | CTA | CGA | AGG | AGG | TTG | ATT | GCA | AAT | CTG | GCT | GAG | CAT | ATT | CTA | 1419 |
| F | T | A | S | K | S | C | A | I | M | S | T | H | I | V | A | C | L | L | L | 493 |
| TTC | ACT | GCT | AGC | AAG | TCC | TGT | GCC | ATT | ATG | TCC | ACA | CAC | ATT | GTG | GCT | TGC | CTG | CTC | CTC | 1479 |
| Y | R | H | R | Q | G | I | D | L | L | S | T | L | V | E | D | F | V | M | K | 513 |
| TAC | AGA | CAC | AGG | CAG | GGA | ATT | GAT | CTC | TCC | ACA | TTG | GTC | GAA | GAC | TTT | TTT | GTG | ATG | AAA | 1539 |
| E | E | V | L | A | R | D | F | D | L | G | F | S | G | N | S | E | D | V | V | 533 |
| GAG | GAA | GTC | GCT | GCT | GAT | TTT | GAC | CTG | GGG | TTC | TCA | GGA | AAT | TCA | GAA | GAT | GTA | GTA | GTA | 1599 |

FIG. 1D

| | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| M | H | A | I | Q | L | L | G | N | C | V | T | I | T | H | T | S | R | N | D | 553 |
| ATG | CAT | GCC | ATA | CAG | CTG | CTG | GGA | AAT | TGT | GTC | ACA | ATC | ACC | CAC | ACT | AGC | AGG | AAC | GAT | 1659 |
| E | F | F | I | T | P | S | T | T | V | P | S | V | F | E | L | N | F | Y | S | 573 |
| GAG | TTT | TTT | ATC | ACC | CCC | AGC | ACA | ACT | GTC | CCA | TCA | GTC | TTC | GAA | CTC | AAC | TTC | TAC | AGC | 1719 |
| N | G | V | L | H | V | F | I | M | E | A | I | I | A | C | S | L | Y | A | V | 593 |
| AAT | GGG | GTA | CTT | CAT | GTC | TTT | ATC | ATG | GAG | GCC | ATC | ATA | GCT | TGC | AGC | CTT | TAT | GCA | GTT | 1779 |
| L | N | K | R | G | L | G | G | P | T | S | T | P | P | N | L | I | S | Q | E | 613 |
| CTG | AAC | AAG | AGG | GGA | CTG | GGG | GGT | CCC | ACT | AGC | ACC | CCA | CCT | AAC | CTG | ATC | AGC | CAG | GAG | 1839 |
| Q | L | V | R | K | A | A | S | L | C | Y | L | L | S | N | E | G | T | I | S | 633 |
| CAG | CTG | GTG | CGG | AAG | GCG | GCC | AGC | CTG | TGC | TAC | CTT | CTC | TCC | AAT | GAA | GGC | ACC | ATC | TCA | 1899 |
| L | P | C | Q | T | F | Y | Q | V | C | H | E | T | V | G | K | F | I | Q | Y | 653 |
| CTG | CCT | TGC | CAG | ACA | TTT | TAC | CAA | GTC | TGC | CAT | GAA | ACA | GTA | GGA | AAG | TTT | ATC | CAG | TAT | 1959 |
| G | I | L | T | V | A | E | H | D | D | Q | E | D | I | S | P | S | L | A | E | 673 |
| GGC | ATT | CTT | ACA | GTG | GCA | GAG | CAC | GAT | GAC | CAG | GAA | GAT | ATC | AGT | CCT | AGT | CTT | GCT | GAG | 2019 |
| Q | Q | W | D | K | K | L | P | E | P | L | S | W | R | S | D | E | E | D | E | 693 |
| CAG | CAG | TGG | GAC | AAG | AAG | CTT | CCA | GAA | CCT | TTG | TCT | TGG | AGA | AGT | GAT | GAA | GAA | GAT | GAA | 2079 |
| D | S | D | F | G | E | E | Q | R | D | C | Y | L | F | V | S | Q | S | K | E | 713 |
| GAC | AGT | GAC | TTT | GGG | GAG | GAA | CAG | CGA | GAT | TGC | TAC | CTG | AAG | GTG | AGC | CAA | TCC | AAG | GAG | 2139 |
| H | Q | Q | F | I | T | F | L | Q | R | L | L | G | P | L | L | E | A | Y | S | 733 |
| CAC | CAG | CAG | TTT | ATC | ACC | TTC | TTA | CAG | AGA | CTC | CTT | GGG | CCT | TTG | CTG | GAG | GCC | TAC | AGC | 2199 |

5/32

FIG. 1E

S A A I F V H N F S G P V P E P E Y L Q 753
 TCT GCT GCC ATC TTT GTT CAC AAC TTC AGT GGT CCT GTT CCA GAA CCT GAG TAT CTG CAA 2259

 K L H K Y L I T R T E R N V A V Y A E S 773
 AAG TTG CAC AAA TAC CTA ATA ACC AGA ACA GAA AAT GTT GCA GTA TAT GCT GAG AGT 2319

 A T Y C L V K N A V K M F K D I G V F K 793
 GCC ACA TAT TGT CTT GTG AAG AAT GCT GTG AAA ATG TTT AAG GAT ATT GGG GTT TTC AAG 2379

 E T K Q K R V S V L E L S S T F L P Q C 813
 GAG ACC AAA CAA AAG AGA GTG TCT GTT TTA GAA CTG AGC AGC ACT TTT CTA CCT CAA TGC 2439

 N R Q K L L E Y I L S F V V L * 829
 AAC CGA CAA AAA CTT CTA GAA TAT ATT CTG AGT TTT GTG GTG CTG TAG 2487

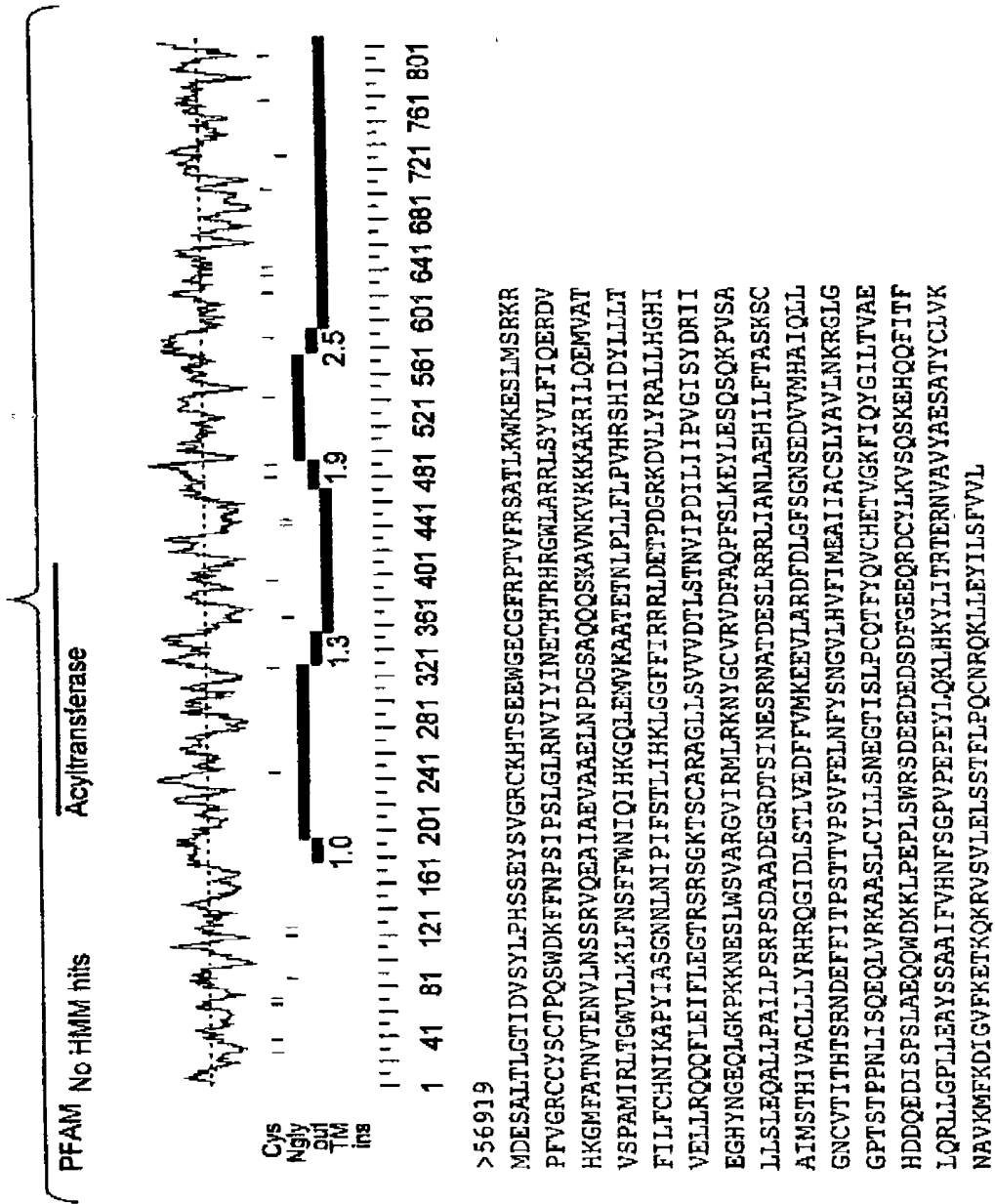
GTAACGTGTGGCAGTCTGCTGGCAATGAGGTCAATGAGTGTGAGTTCCTTTGTAGGTACCAAGCTTCTGCTCAAGAGTTTGA

AGGTGCTTTCGACAGGGTCAGGCTGCTGTCNCCGAGTGAATCTCTGGAGAGACAAGTGCCTTCTNCTCCATGGATC

TGAGATCTTCCAGCTTT

6/32

FIG. 2



7/32

FIG. 3A

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine

HMMER is freely distributed under the GNU General Public License (GPL).

HMM file:

/prod/ddm/seganal/pfam6.4/pfam

Sequence file:

/prod/ddm/wspace/orfanel/oa-script.21255.seq

Query: 56919

Scores for sequence family classification (score includes all domains):

| Model | Description | Score | E-value | N |
|-----------------|-----------------|-------|---------|---|
| Acyltransferase | Acyltransferase | 126.1 | 6.4e-34 | 1 |

Parsed for domains:

| Model | Domain | seq-f | seq-t | hmm-f | hmm-t | score | E-value |
|-----------------|--------|-------|--------|-------|--------|-------|---------|
| Acyltransferase | 1/1 | 215 | 412 .. | 1 | 195 {} | 126.1 | 6.4e-34 |

8/32

FIG. 3B

Alignments of top-scoring domains:

Acyltransferase: domain 1 of 1, from 215 to 412: score 126.1, E = 6.4e-34

*->lenlpkkgaipvvsNHRsYlDilvlsaalprrgplvrvlrvfiakke

+ +++++ p ++ + HRS+D+1+1 ++l++++ ++ +ia ++

56919 215 KAATETNLPFLFVHRSHIDYLLTFFILFCHN-----IKAPYIASGN 257

llkvPllfGwlmrlagafidRmra.....kdalaaadelvrvlellrk

+l++P+ f++l+ ++g +fi+R+ ++++++kd l++a+ + + tellr+

56919 258 NINIPi-FSTLIHKLGGFFIRRLDEtpdgrKDVLYRALLGHIVELLRQ 306

grsvliFPEGTRrsrgellppfKkGia.....afrlAlkagvpivPvviv

+ + iF EGTRsrg++ + +G++ + + ++ ++ i+Pv+i

56919 307 QQFLElFLEGTRSRSGKTSC-ARAGLLsvvvdTLSTNVIPDILIIIPVGI- 354

sgreelepknagkllrlarkkgpvtvrvlppipld..pedikelaerlr

s++ ++e +++ + ++++++ v +++ +++++ +

56919 355 SYDRlIEGHYNCEQ--LGKPKNESlMSVARGVIRMIRKNYSCVRVDFQA 402

dilvqaleel<*

+ ++++ e+

56919 403 PPSLKEYLES 412

9/32

FIG. 4A

| ProDom Matches ProDomId | Start | End | Description | Score |
|----------------------------|-------|-----|---|-------|
| View Prodom PD347660 | 1 | 55 | p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL | 250 |
| View Prodom PD087501 | 51 | 158 | p2001.1 (1) // AIP2-DLD1 | 77 |
| View Prodom PD353731 | 56 | 152 | p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL | 500 |
| View Prodom PD037846 | 128 | 259 | p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR MITOCHONDRION | 258 |
| View Prodom PD042466 | 259 | 590 | p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE MITOCHONDRION | 413 |
| View Prodom PD025192 | 462 | 649 | p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION | |

10/32

FIG. 4B

458

View Prodom PD042027 465 673 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE
GLYCEROL-3-PHOSPHATE MEMBRANE
PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT

80

View Prodom PD042760 650 828 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE
PHOSPHOLIPID BIOSYNTHESIS PRECURSOR
TRANSMEMBRANE GLYCEROL-3-PHOSPHATE
GPAT MITOCHONDRION MITOCHONDRIAL

799

View Prodom PD042760

>PD042760 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
MITOCHONDRIAL

Length = 179

Score = 799 (286.3 bits), Expect = 1.2e-79, P = 1.2e-79
Identities = 155/179 (86%), Positives = 161/179 (89%)

Query: 650 FIQYGILTVAEHDDQEDISPSLAEQQWDKKLPELSWRXXXXXXXXXXXXXQORDCYLKVS 709
FIQYGILTVAE DDQED+SP LAEQQW+KKLPEPL+WR QORDCYLKVS

Sbjct: 1 FIQYGILTVAEQDDQEDVSPGLAEQQWKKLPEPLNWRSEDEDESDFGEEQORDCYLKVS 60

Query: 710 QSKEHQQFITFLQRLGLPLLEAYSSAAIFVHNFGVPPEPEYLOKLHKYLIITRERNVAV 769
Q+KEHQQFITFLQRLGLPLLEAYSSAAIFVHNF GPVPE EYLOKLH+YLIITRERNVAV

Sbjct: 61 QAKEHQQFITFLQRLGLPLLEAYSSAAIFVHNFRGPVPESEYLOKLHRYLIITRERNVAV 120

Query: 770 YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELSSTFLPQCNRQKLLLEYILSFVVL 828
YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELS+TFPLPQCNRQKLLLEYILSFVVL

Sbjct: 121 YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELSSTFLPQCNRQKLLLEYILSFVVL 179

11/32

FIG. 4C

View Prodom PD353751

>PD353751 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
 MITOCHONDRION

Length = 97

Score = 500 (181.1 bits), Expect = 2.1e-47, P = 2.1e-47
 Identities = 90/97 (92%), Positives = 97/97 (100%)

Query: 56 MSKRPFVGRCCYCTPQSWDKFFNPSPISGLRNVIYINETHTRHGWLARRLSYVLF 115
 MSKRPFVGRCCYCTPQSW++FFNPSPISGLRNVIYINETHTRHGWLARRLSY+LF+
 Sbjct: 1 MSKRPFVGRCCYCTPQSWERFFNPSPISGLRNVIYINETHTRHGWLARRLSYILFV 60

Query: 116 QERDVHKGMFATNVNTENLNSSRVQEAIAEVAELNP 152
 QERDVHKGMFAT++T+NVLNSSRVQEAIAEVAELNP
 Sbjct: 61 QERDVHKGMFATSITDNLNSSRVQEAIAEVAELNP 97

View Prodom PD025192

>PD025192 p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRION
 BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT
 MITOCHONDRION

Length = 194

Score = 458 (166.3 bits), Expect = 8.7e-43, P = 8.7e-43
 Identities = 95/192 (49%), Positives = 126/192 (65%)

Query: 462 RRLIANLAEHILFTASKSCAISMTHIVACLLYRHRQIDLSLTVEDFFVMKEEVLARDF 521
 R LI ++ EH++F S C+INSTH+VACLLL R R G+ STL ED + E++LA
 Sbjct: 3 RNLIRSIGEHVVFDCSMNCISMTHVACLLITRWNGVHRSTLEEDCDNLCEKILAEFG 62

12/32

FIG. 4D

Query: 522 DL-GFSGNS---EDVVMHAIQLGNCVTITHTSRNDEFFITPSTTVPSVFELNFSNGVL 577
 D+ GFSG S +V +A +LLG+CVT+T RNDEF+I+P +VPS EL +YSN V+
 Sbjct: 63 DIVGFSGCKSTKGSQIVKYACELLGSCVTVTDEDRNDEFYISPKNSVPSFIELAYVNSVI 122

Query: 578 HVFIMEAIIACSLYAVLNKRGGLGPTSTPPNLIQEQQLVRKAASLCYLLSNEGTSILPCQ 637
 F +++IIAC++Y++ NK GG NLISQEQLV A SLG L E PCQ
 Sbjct: 123 CHFALKSIIACTIYSLPNKTKNGGAGGLNLISQEQQLVEDALSICDMLQVEFMFCRPCQ 182

Query: 638 TFYQVCHETVGK 649
 T ++CH T+GK
 Sbjct: 183 TLRELCHNTLIGK 194

View Prodom PD042466

>PD042466 p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
 BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE
 MITOCHONDRION
 Length = 299

Score = 413 (150.4 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42
 Identities = 79/152 (51%), Positives = 108/152 (71%)

Query: 259 LNIPFSTLIHKLGGFFIRRLDETPDGRKDVLYRALLHGHIVELLRQQQFLEIFLEGTR 318
 L++PI +L+ + G FFIRR D TP+G+ D LYRA+ H ++ +L+ + +E F+EGTR
 Sbjct: 2 LSMPTMGSLLRRTGAFFIRRSFDPTECKGQDLYRAVFHEVYVAQLISKGYNIEFFIEGTR 61

Query: 319 SRSKTSICARAGLLSVVVDTLSTNVIPDILLIPVGISYDRIIEGH-YNGEQLGKPKKNES 377
 SR+GK + GLLS+VV+ +PDIL++PV ISYDRIIEG+ Y E G PKK ES
 Sbjct: 62 SRTGKNLPKTKGLLSMVVEAFLRGSVPDILLVPVSIYDRIIEGNTYAHELRGAPKKES 121

13/32

FIG. 4E

Query: 378 LMSVARGVIRMLRKNYGVVRVDFQAQPSLKEY 409
 LM + RGV +ML++NYG V VDF +P SL+EY
 Sbjct: 122 LMQFRGVRRMLKRNQGVYVDFGEPISLREY 153

Score = 64 (27.6 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42
 Identities = 30/143 (20%), Positives = 59/143 (41%)

Query: 453 RNATDESIRRRLLIANLAHILFTASKSCAIMSTHIVACLLLYRHRQSIDLSTL---VEDF 509
 RN + + +R + + + + + + + + + +T +V+ LLL + L L ++D
 Sbjct: 160 RNTYNCAPKRLALQKMSFEVAVRILQATPVTATGLVSALLLTTRGTALTLDQLHHTLQDS 219

Query: 510 FVMKEVLAROFDLGFGNSDVMVHAIQLL--GNCVTITHTSRNDEFFITPSTTVPSVF 567
 E + S + V A L G+ VT + R ++I P + F
 Sbjct: 220 LDYLERKQSPVSTSLRLRSREGVRAADALSNGHPVTRVDSGHEPVWYIAPDDEHAAAF 279

Query: 568 ELNPFYSGVLHVFMELIACSL 590
 Y N V+H F+ +I+ +L
 Sbjct: 280 -----YRNSVIHAFLETSIVELAL 298

View Prodom PD037846

>PD037846 p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
 PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR
 MITOCHONDRION
 Length = 345

Score = 258 (95.9 bits), Expect = 3.4e-21, P = 3.4e-21
 Identities = 56/132 (42%), Positives = 79/132 (59%)

14/32

FIG. 4F

Query: 128 NVTENVLNSSRVQEAIAEVAELNPDGSAQQSQSXXXXXXXXXXXXXRIQEMVATVSPAMIR 187
 N+ +NVLNS + I + A++ S IL EM T++ MIR
 Sbjct: 223 NLKKNVLNSEEIHYVIEQ-----EAKESSTSIDKVRREAREILDEMSHTLNMGNIR 273

Query: 188 LTGWLLKLFNSFFWNIQHKQLEMVKAATETNLPLFLPVHRSHIDYLLLTFLFCHN 247
 GWVL K+FN F I +++ Q+E +K ATE P+++LP HRSHIDYLLL+FIL+ ++
 Sbjct: 274 FCGWVLSKIFNRIFSGICVNEEQIEKIKRATEQGHPIYLPSPHRSHIDYLLLSFILLHYD 333

Query: 248 IKAPYIASGNL 259
 IK P+IA+G NL
 Sbjct: 334 IKVPHIAAGMNL 345

View Prodom PD347660

>PD347660 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
 MITOCHONDRIAL
 Length = 55

Score = 250 (93.1 bits), Expect = 2.4e-20, E = 2.4e-20
 Identities = 43/55 (78%), Positives = 53/55 (96%)

Query: 1 MDESALTIGTIDVSYLPSPSEYSVGRCKHTSEWGEQGFPTVFRSATLKWKESL 55
 M+ES++T+GTIDVSYLP+SSEYS+GRCKHT+E+W +CGF+PT FRSATLKWKESL
 Sbjct: 1 MEESVITIGTIDVSYLPNSSEYSLGCKHTNEDWDVDCGFKPTFRSATLKWKESL 55

15/32

FIG. 4G

View Prodom PD042027

>PD042027 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE
 PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT
 Length = 345

Score = 80 (33.2 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 31/129 (24%), Positives = 60/129 (46%)

Query: 465 IANLAEHILFTASKSCAIMSTHIVACLLLYRHRQGIDLSTLVE--DFFVMKEEVLARDFD 522
 + +LA+ I+ + + A+ ++ A LL ++ + L+E D ++ + D

Sbjct: 32 VNHLAKQIMTHINDAAAVNPNMLCATALLSTRQALGEEQLIEQLDCYLKLLRNVPYSTD 91

Query: 523 LGFSGNS-EDVVMHAIQ--LLGNCVTITHTSRNDEFFITPSTVPSELNPFYNSGVHLV 579
 ++ E ++ HA Q LLG VT+ + D + V + +Y N VLN+

Sbjct: 92 ATLDPHTPERLIEHAEQMNLLG--VTVEKDTLGDILRLDRDNAVL-----MTYYRNNVNLHL 145

Query: 580 FIMEAIIAC 588
 F + A++AC

Sbjct: 146 FALPALVAC 154

Score = 62 (26.9 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 22/105 (20%), Positives = 48/105 (45%)

Query: 569 LNFYSNGVLHVFIEMAIACSLYAVLNKRGLGPGTTPPNLISQQLVKAASLCYLLSN 628
 + +Y N VLN+ F + A++AC N+R IS++ L+R +L L

Sbjct: 135 MTYYRNNVNLHIFALPALVACCFKN--NRR-----ISRDAIIRFVRALYPFLQA 180

Query: 629 EGTISLPCQTFYQVCHETVGVKFIQYGILTVAEHDDQEDISPSLAE 673
 E + + + +F++ G+L A + + + ++ + ++

Sbjct: 181 ELFLRWNEDELNDHIDQWINEFVRQGLLSAGNQEDDTLFRNTSQ 225

16/32

FIG. 4H

View Prodom PD087501

>PD087501 p2001.1 (1) // AIP2-DLD1
Length = 170

Score = 77 (32.2 bits), Expect = 5.1, P = 0.994
Identities = 31/114 (27%), Positives = 44/114 (38%)

Query: 51 WKES--LMSRRPFVGRCCYCTPQSNDEKFFNPSISLGLRNVIYINETHTRHRCGLARR 108

W ES L+ RK F RCC F K + L N +H W

Sbjct: 12 WNESEVLVDRKSKFOARCC----PLQXQKDIPSILQELTONKNSVSKASHMHMYAWRTAE 67

Query: 109 LSYVLFIQERDVHKGFMFATNVTVENVLN SSR--VQ-EAIAEVAELNPDGSAQQ 158

+S L +Q+ KG A + +N SR VQ + I + A+ G+ Q+

Sbjct: 68 VSNLHLQQEQKKKGKANKNSNNSHVKNKSRNITVQPKNIEQGCADCGEAGAGOR 121

17/32

FIG. 5A

| | | | | | |
|-----|---------|------|-----------------------------------|---------------|--|
| | 10 | 20 | 30 | 40 | |
| 1 | MDESALT | LG | TIDVSYLPHSSEYSVGRCKHTSEEWGECGFR | 56919.pro | |
| 1 | MEESSVT | VTG | TIDVSYLPSSEYSVGRCKHTSEDWVDCGFK | MouseGPAT.PRO | |
| 1 | MEESSVT | TIG | TIDVSYLPSSEYSVGRCKHTNEDWVDCGFK | RatGPAT.PRO | |
| | 50 | 60 | 70 | 80 | |
| 41 | PTVFRS | ATL | KWKESLMSRKRPFVGRCCYSCTPQSWDKFFN | 56919.pro | |
| 41 | PTFFRS | ATL | KWKESLMSRKRPFVGRCCYSCTPQSWERFFN | MouseGPAT.PRO | |
| 41 | PTFFRS | ATL | KWKESLMSRKRPFVGRCCYSCTPQSWERFFN | RatGPAT.PRO | |
| | 90 | 100 | 110 | 120 | |
| 81 | PSIPSL | GLRN | VIYINETHTRHRGWLARRLSYVLFQERDV | 56919.pro | |
| 81 | PSIPSL | GLRN | VIYINETHTRHRGWLARRLSYILFVQERDV | MouseGPAT.PRO | |
| 81 | PSIPSL | GLRN | VIYINETHTRHRGWLARRLSYILFVQERDV | RatGPAT.PRO | |
| | 130 | 140 | 150 | 160 | |
| 121 | HKGMF | ATN | VTENVLNSSSRVQEATAEVAAELNPDGSAQQQS | 56919.pro | |
| 121 | HKGMF | ATN | VTENVLNSSSRVQEATAEVAAELNPDGSAQQQS | MouseGPAT.PRO | |
| 121 | HKGMF | ATN | VTENVLNSSSRVQEATAEVAAELNPDGSAQQQS | RatGPAT.PRO | |
| | 170 | 180 | 190 | 200 | |
| 161 | KAVNK | VKKK | KAKRILOEMVATVSPAMIRLTGWVLLKLFNSF | 56919.pro | |
| 161 | KAIQK | VKKR | KARKILOEMVATVSPGMIRLTGWVLLKLFNSF | MouseGPAT.PRO | |
| 161 | KAIQK | VKKR | KARKILOEMVATVSPGMIRLTGWVLLKLFNSF | RatGPAT.PRO | |
| | 210 | 220 | 230 | 240 | |
| 201 | FWNIQ | IHK | GOLEMVKAATETNLPILFLPVHRSHIDYLLLT | 56919.pro | |
| 201 | FWNIQ | IHK | GOLEMVKAATETNLPILFLPVHRSHIDYLLLT | MouseGPAT.PRO | |
| 201 | FWNIQ | IHK | GOLEMVKAATETNLPILFLPVHRSHIDYLLLT | RatGPAT.PRO | |
| | 250 | 260 | 270 | 280 | |
| 241 | FILECH | NIK | KAPYIASGNNLNIPFSTLIHKLGGFFIRRRRL | 56919.pro | |
| 241 | FILECH | NIK | KAPYIASGNNLNIPVSTLIHKLGGFFIRRRRL | MouseGPAT.PRO | |
| 241 | FILECH | NIK | KAPYIASGNNLNIPFSTLIHKLGGFFIRRRRL | RatGPAT.PRO | |
| | 290 | 300 | 310 | 320 | |
| 281 | DETPD | GRK | DVLYRALLHGHIVELLRQQQFLEIFLEGTRSR | 56919.pro | |
| 281 | DETPD | GRK | DVLYRALLHGHVVELLRQQQFLEIFLEGTRSR | MouseGPAT.PRO | |
| 281 | DETPD | GRK | DVLYRALLHGHIVELLRQQQFLEIFLEGTRSR | RatGPAT.PRO | |
| | 330 | 340 | 350 | 360 | |
| 321 | SGKT | SCAR | AGLLSVVVDTLSTNVIPDILIPVGISYDRII | 56919.pro | |
| 321 | SGKT | SCAR | AGLLSVVVDTLSSNTIPDILIPVGISYDRII | MouseGPAT.PRO | |
| 321 | SGKT | SCAR | AGLLSVVVDTLSSNTIPDILIPVGISYDRII | RatGPAT.PRO | |

18/32

FIG. 5B

| | | | | | |
|-----|--|-----|-----|-----|---------------|
| | 370 | 380 | 390 | 400 | |
| 361 | EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGCVRVDF | | | | 56919.pro |
| 361 | EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF | | | | MouseGPAT.PRO |
| 361 | EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF | | | | RatGPAT.PRO |
| | 410 | 420 | 430 | 440 | |
| 401 | AQPFSLKEYLESQSQKPVSAALLSLEQALLPAILPSRPSDA | | | | 56919.pro |
| 401 | AQPFSLKEYLEGQSQKPVSAPLSLEQALLPAILPSRPNDV | | | | MouseGPAT.PRO |
| 401 | AQPFSLKEYLEGQSQKPVSAPLSLEQALLPAILPSRPDAA | | | | RatGPAT.PRO |
| | 450 | 460 | 470 | 480 | |
| 441 | ADEGRDTSINESRNATDESLRRRLIANLAEHILFTASKSC | | | | 56919.pro |
| 441 | ADEHQDLSINESRNPADEAFRRRLIANLAEHILFTASKSC | | | | MouseGPAT.PRO |
| 441 | AAEHEDMSINESRNAADEAFRRRLIANLAEHILFTASKSC | | | | RatGPAT.PRO |
| | 490 | 500 | 510 | 520 | |
| 481 | AIMSTHIVACLLLYRHRQGIIDLSTLVEDFFVMKEEV LARD | | | | 56919.pro |
| 481 | AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEV LARD | | | | MouseGPAT.PRO |
| 481 | AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEV LARD | | | | RatGPAT.PRO |
| | 530 | 540 | 550 | 560 | |
| 521 | FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRNDEFFITPS | | | | 56919.pro |
| 521 | FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS | | | | MouseGPAT.PRO |
| 521 | FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS | | | | RatGPAT.PRO |
| | 570 | 580 | 590 | 600 | |
| 561 | TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVLNKRGLG | | | | 56919.pro |
| 561 | TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVLNKRCSG | | | | MouseGPAT.PRO |
| 561 | TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVQNKRGS | | | | RatGPAT.PRO |
| | 610 | 620 | 630 | 640 | |
| 601 | GPTSTPPNLISQEQLVRKAASLCYLLSNEG TISLPCQTFY | | | | 56919.pro |
| 601 | GPTSTPPNLISQEQLVRKAASLCYLLSNEG TISLPCQTFY | | | | MouseGPAT.PRO |
| 601 | GPTSTPPNLISQEQLVRKAASLCYLLSNEG TISLPCQTFY | | | | RatGPAT.PRO |
| | 650 | 660 | 670 | 680 | |
| 641 | QVCHETVGKFIQYGILTVAEHDDQEDISPSLAEQQWDKKL | | | | 56919.pro |
| 641 | QVCHETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWDKKL | | | | MouseGPAT.PRO |
| 641 | QVCQETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWNKKL | | | | RatGPAT.PRO |
| | 690 | 700 | 710 | 720 | |
| 681 | PEPLSWRSDEEDEDSDFGEEQRDCYLKVSQSKEHQOFITF | | | | 56919.pro |
| 681 | PE-LNWSRSDEEDEDSDFGEEQRDCYLKVSQSKEHQOFITF | | | | MouseGPAT.PRO |
| 681 | PEPLNWSRSDEEDEDSDFGEEQRDCYLKVSQAKEHQOFITF | | | | RatGPAT.PRO |

19/32

FIG. 5C

| | | | | | |
|-----|---|-----|-----|-----|---------------|
| | 730 | 740 | 750 | 760 | |
| 721 | LQRLLGPLLEAYSSAAIFVHNFSGPVPEPEY LQKLHKYLI | | | | 56919.pro |
| 721 | LQRLLGPLLEAYSSAAIFVHNFSGPVPEPEY LQRLHKYLI | | | | MouseGPAT.PRO |
| 721 | LQRLLGPLLEAYSSAAIFVHTFRGPVPEPEY LQRLHKYLI | | | | RatGPAT.PRO |
| | 770 | 780 | 790 | 800 | |
| 761 | TRTERNVAVYAESATYCLVKNVAVKMFKDIGVFKETKQKRV | | | | 56919.pro |
| 761 | TRTERNVAVYAESATYCLVKNVAVKMFKDIGVFKETKQKRV | | | | MouseGPAT.PRO |
| 761 | TRTERNVAVYAESATYCLVKNVAVKMFKDIGVFKETKQKRA | | | | RatGPAT.PRO |
| | 810 | 820 | | | |
| 801 | SVLELSSTFLPQCNRQKLLEYILSFVVL | | | | 56919.pro |
| 801 | SVLELSSTFLPQCNRQKLLEYILSFVVL | | | | MouseGPAT.PRO |
| 801 | SVLELSSTFLPQCNRQKLLEYILSFVVL | | | | RatGPAT.PRO |

20/32

FIG.6

Acyltransferase catalytic motif-I

| | |
|-----------|---------------|
| IFLEGTRSR | 56919.pro |
| IFLEGTRSR | MouseGPAT.PRO |
| IFLEGTRSR | RatGPAT.PRO |
| YFVEGGRSR | EcoliGPAT.PRO |

Acyltransferase catalytic motif-II

| | |
|--------|---------------|
| HRSHID | 56919.pro |
| HRSHID | MouseGPAT.PRO |
| HRSHID | RatGPAT.PRO |
| HRSHMD | EcoliGPAT.PRO |

Acyltransferase catalytic motif-III

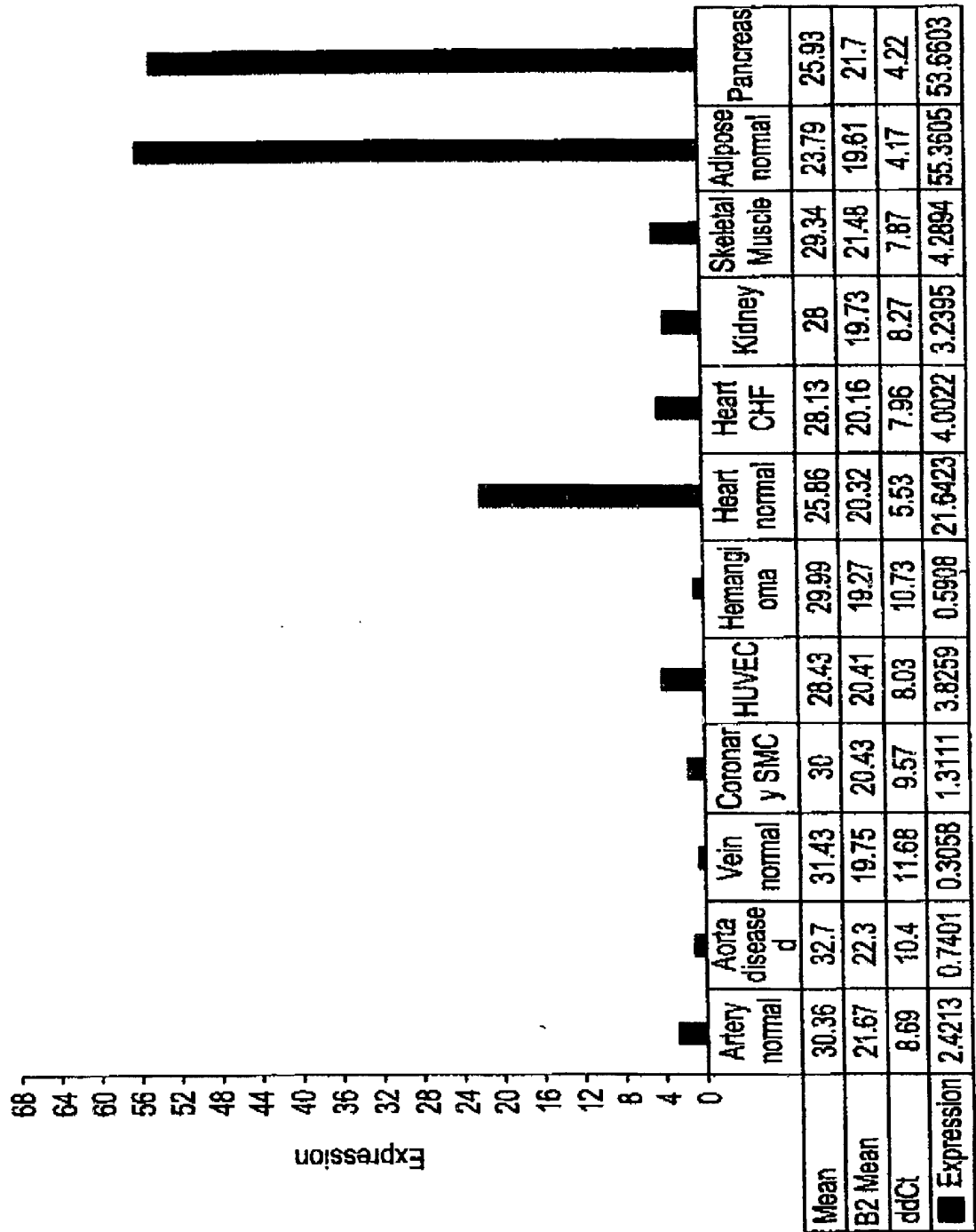
| | |
|--------|---------------|
| ILIIPV | 56919.pro |
| ILVIPV | MouseGPAT.PRO |
| ILVIPV | RatGPAT.PRO |
| ITLIPI | EcoliGPAT.PRO |

Acyltransferase signature motif

| | |
|---------|---------------|
| GGFFIRR | 56919.pro |
| GGFFIRR | MouseGPAT.PRO |
| GGFFIRR | RatGPAT.PRO |
| GAFFIRR | EcoliGPAT.PRO |

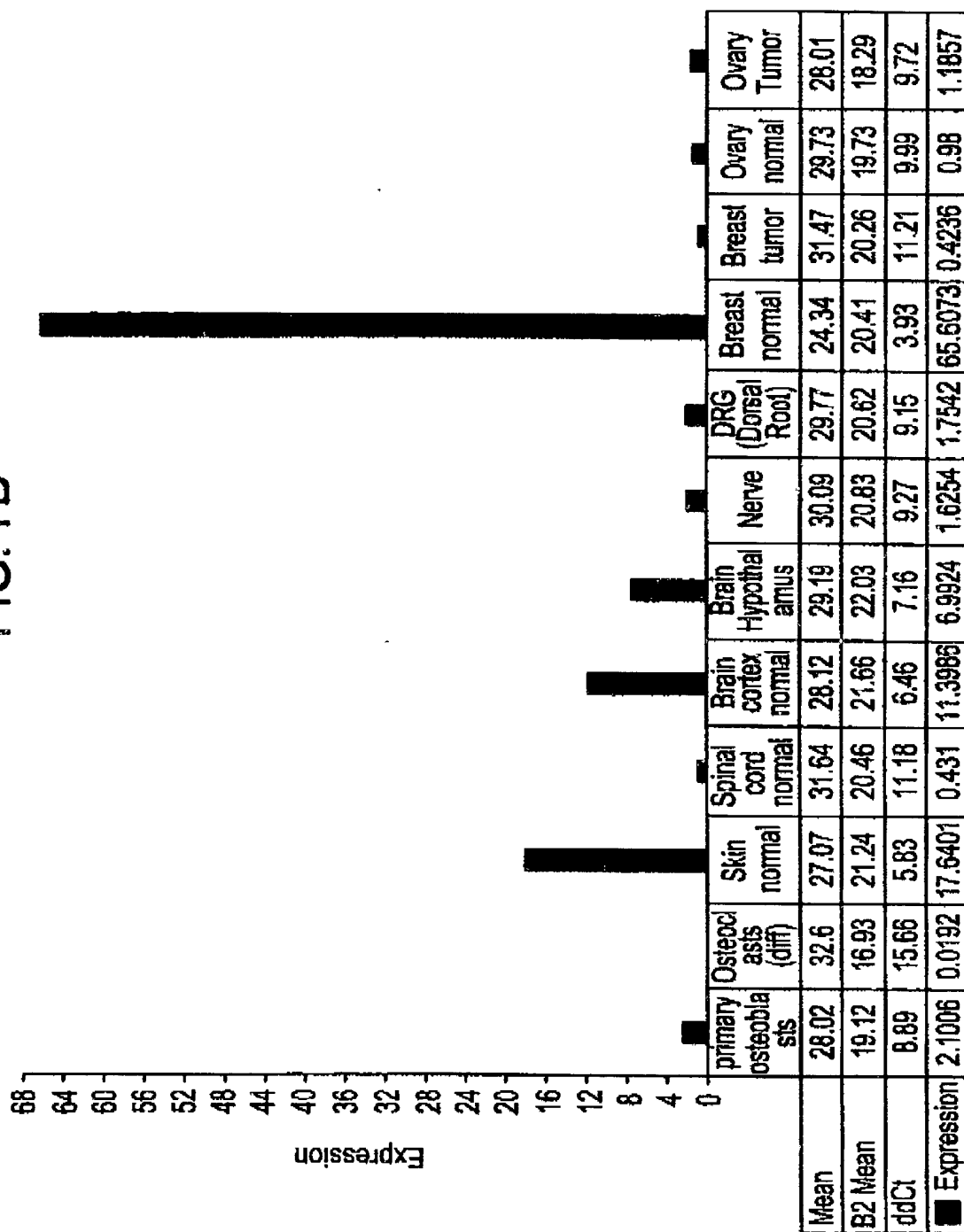
21/32

FIG. 7A



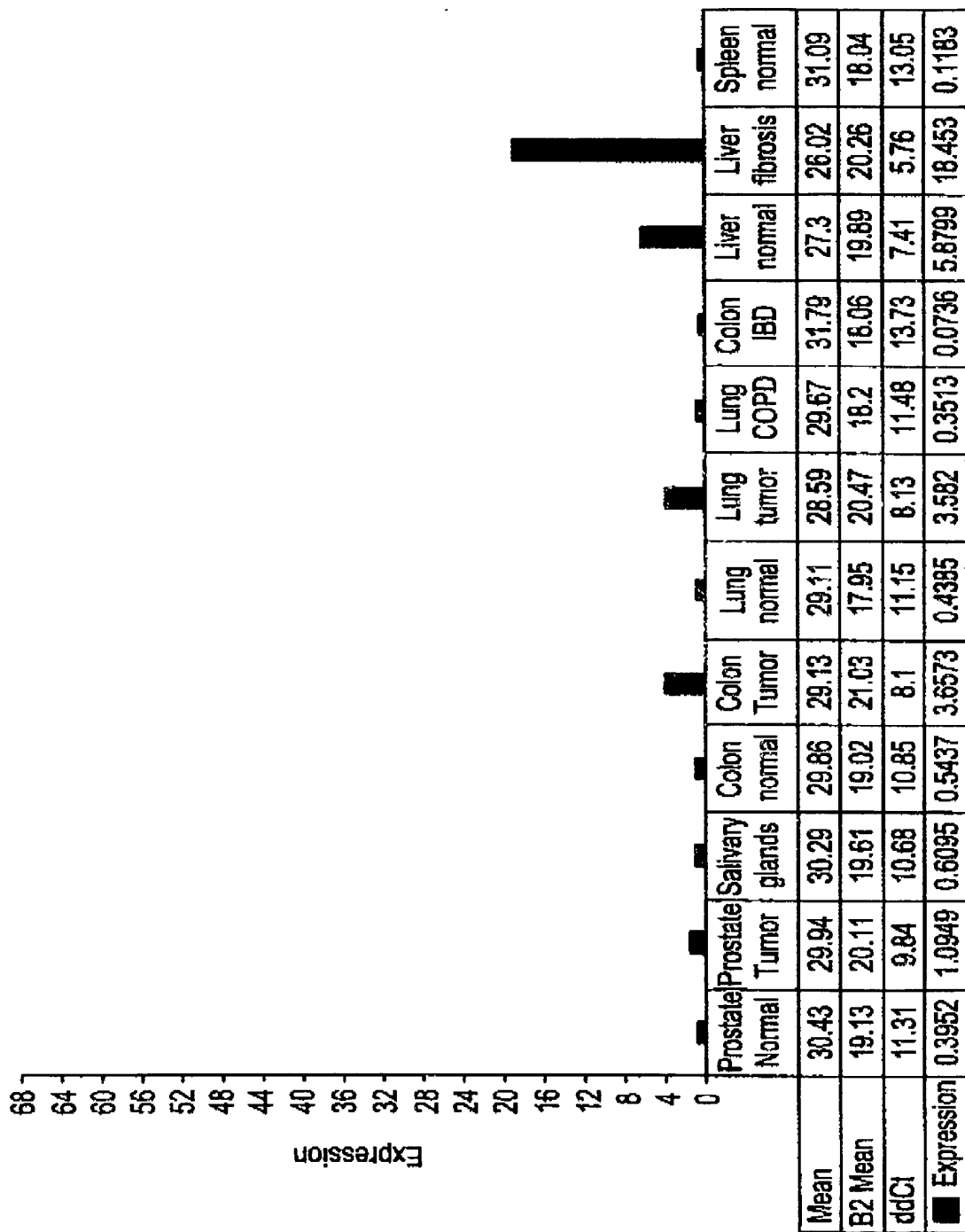
22/32

FIG. 7B



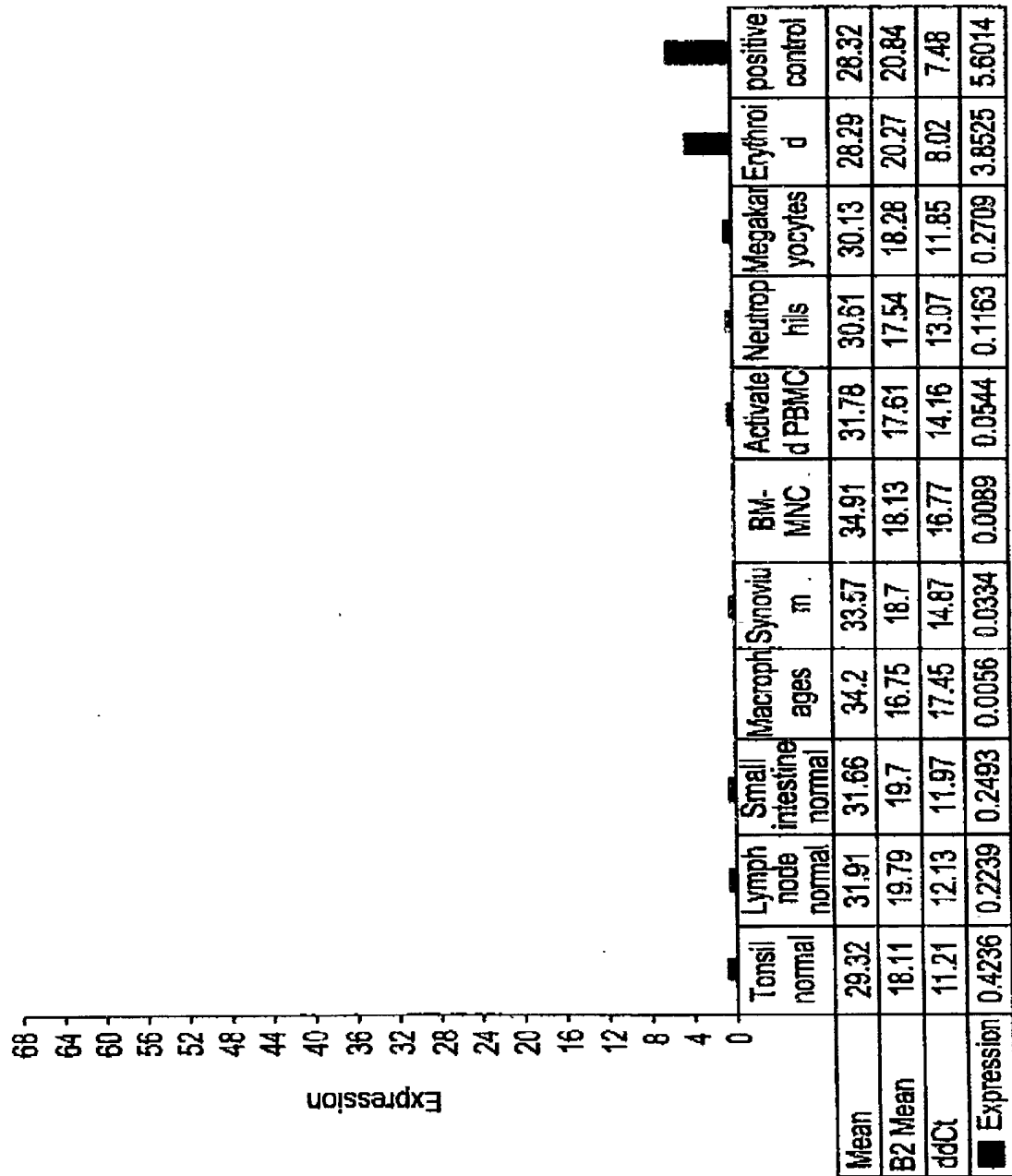
23/32

FIG. 7C



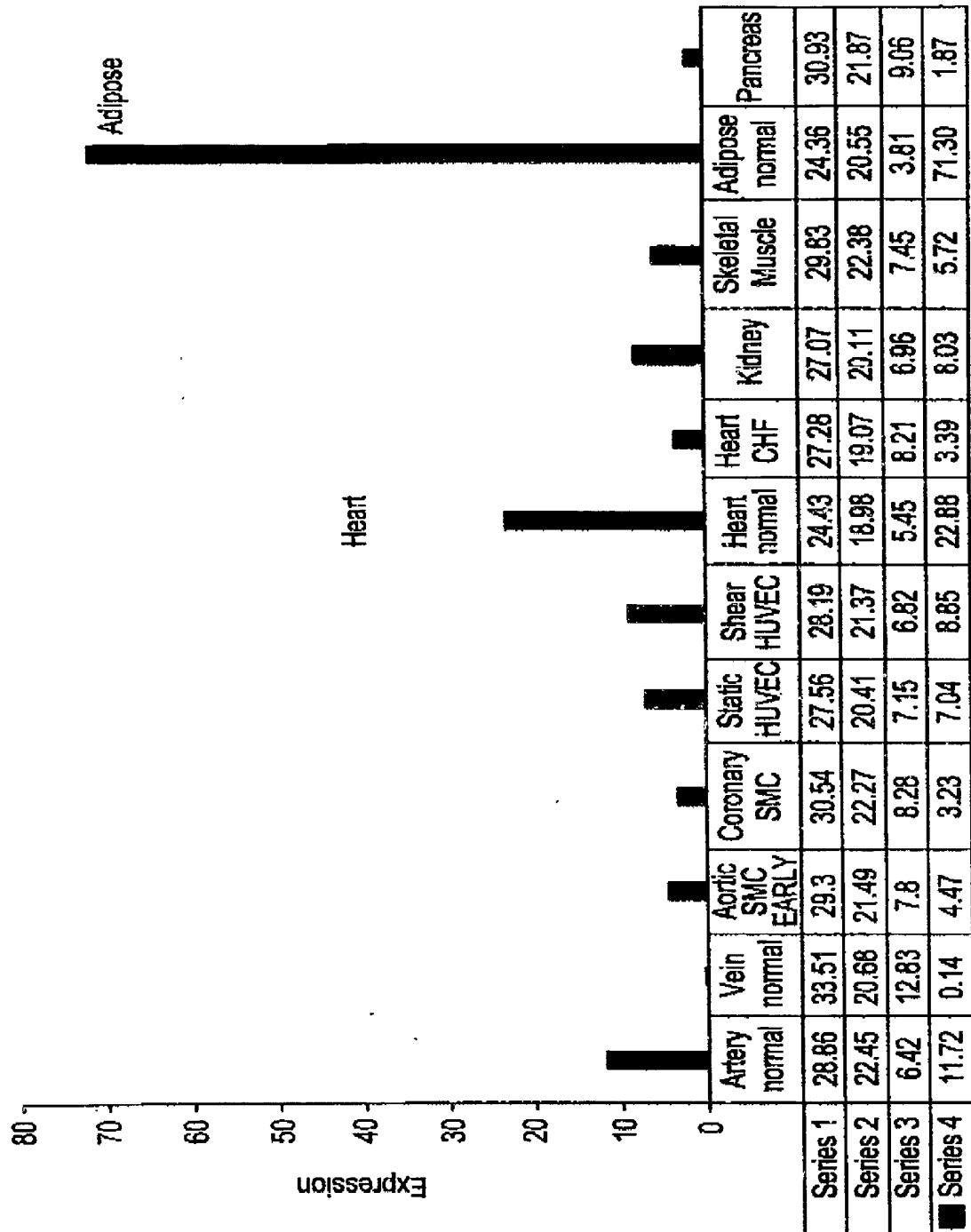
24/32

FIG. 7D



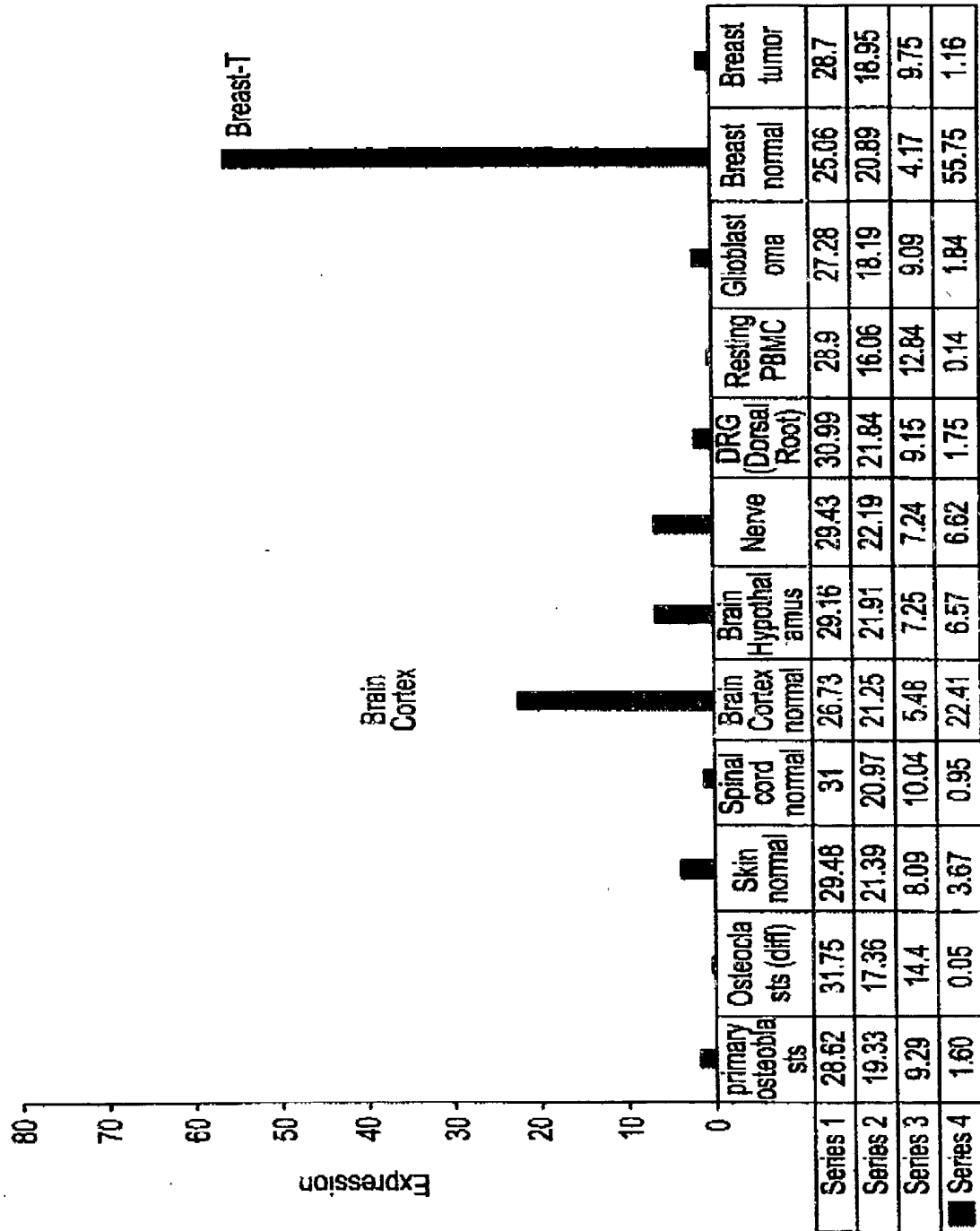
25/32

FIG. 8A



26/32

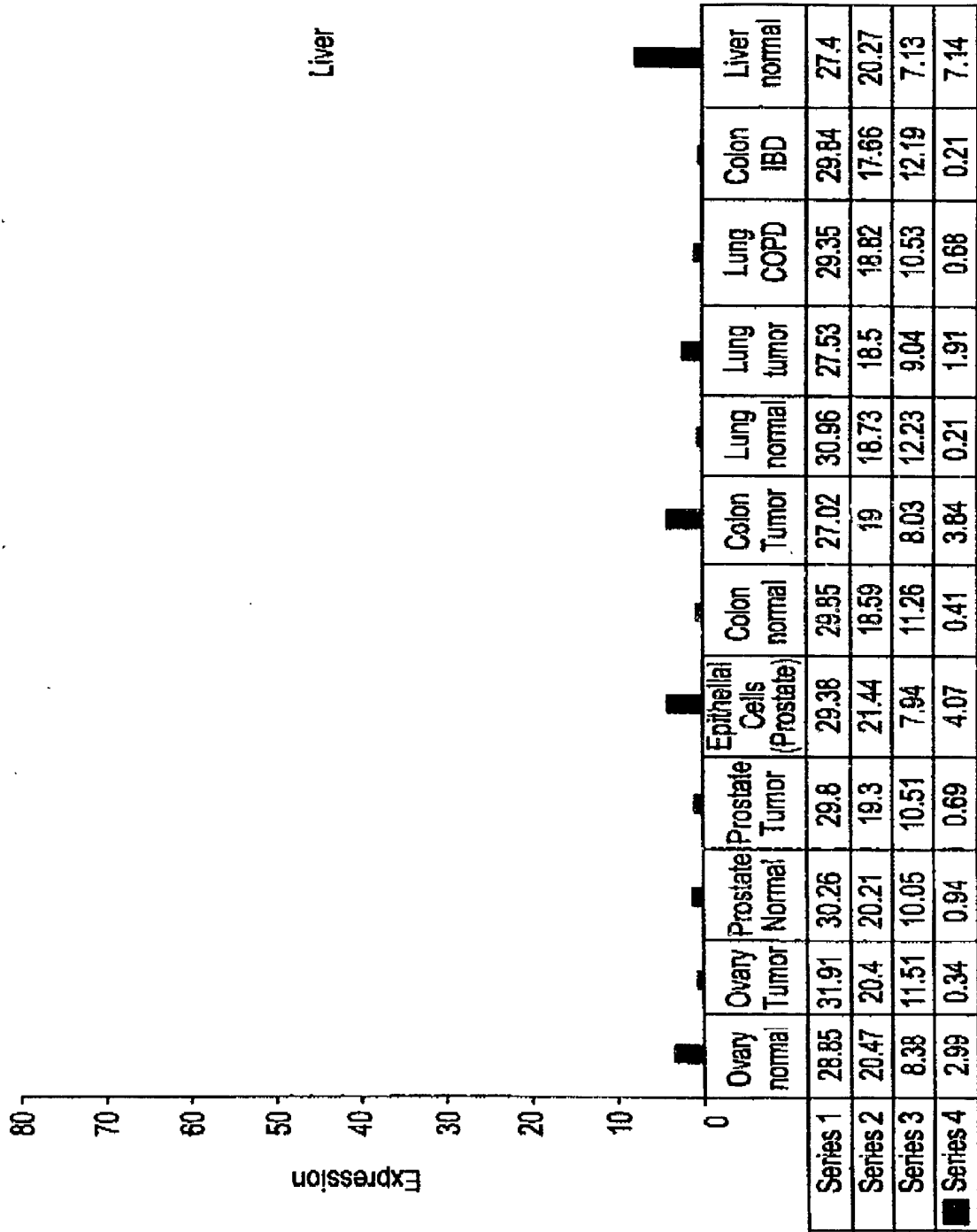
FIG. 8B



27/32

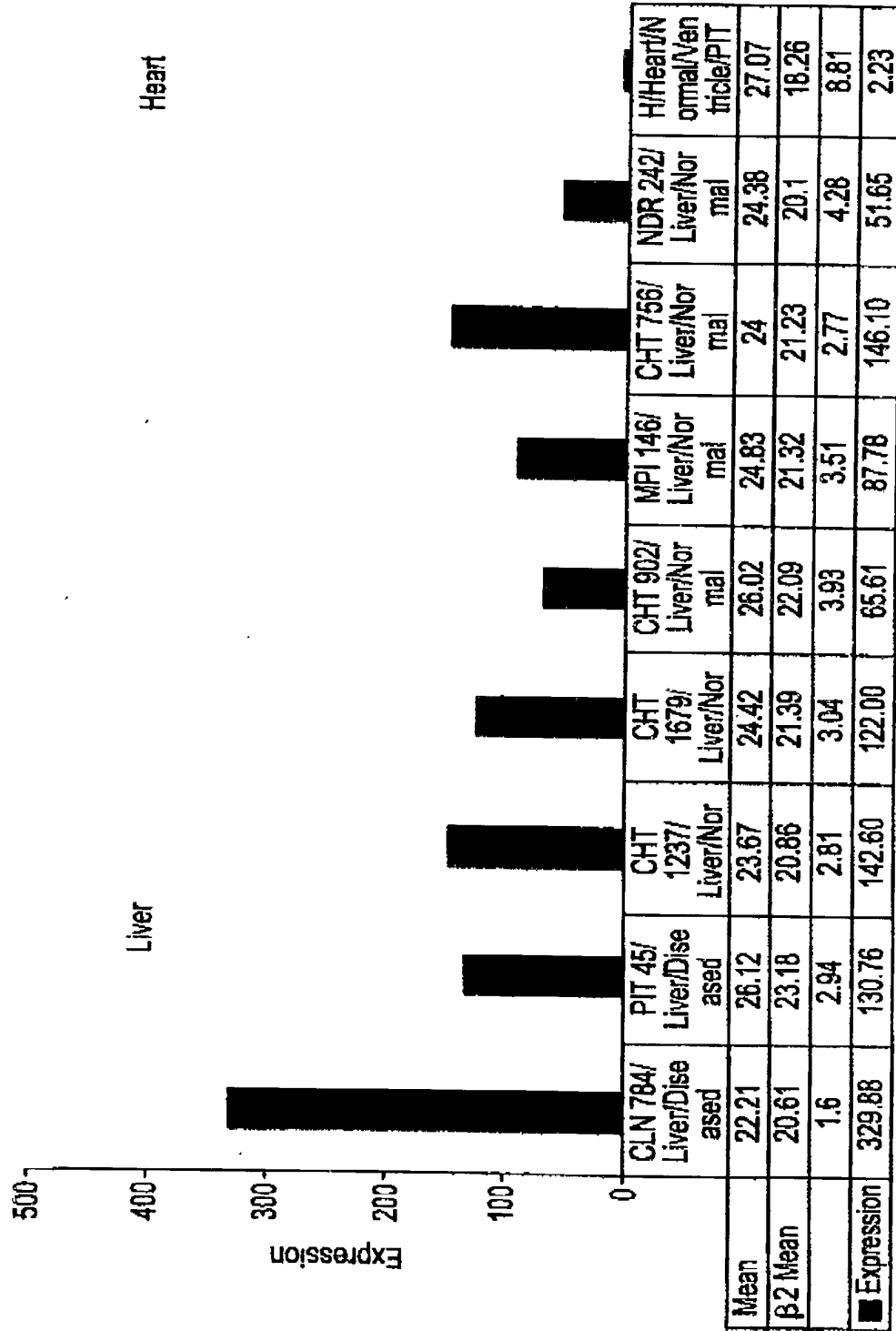
Liver

FIG. 8C



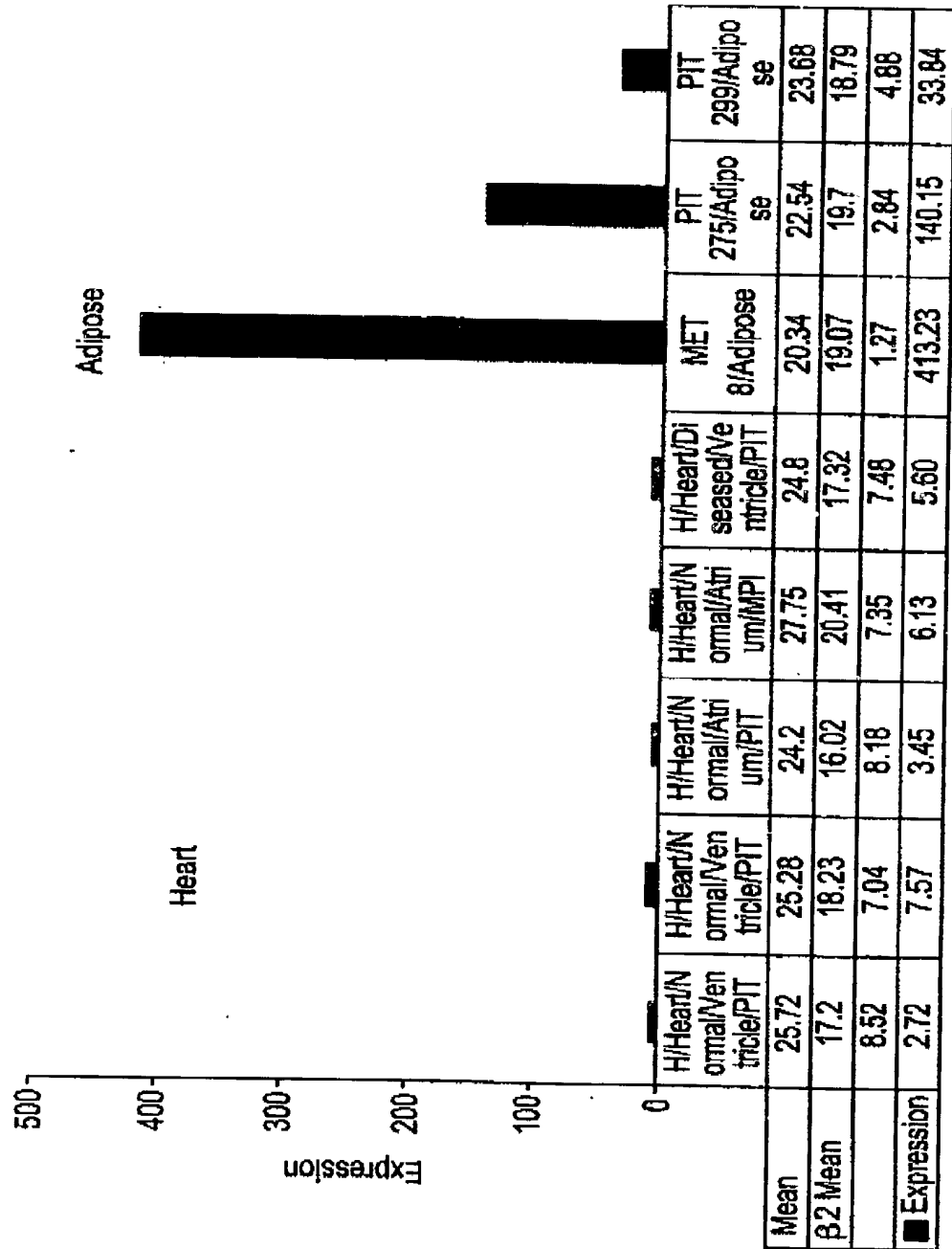
29/32

FIG. 9A



30/32

FIG. 9B



32/32

FIG. 10B

